Supplementary Statistics S1: Propensity Score.

Missing Data: We evaluated the rates of missing data in the majority was less than 10%. The smoking variable presented with 21.3% missing (Supplementary Table S1).

Propensity score matching: We used propensity score matching to estimate the effect of the treatment with convalescent plasma on COVID-19 transplant patients accounting for confounding by the included covariates. We included in match the variables associated with COVID prognosis by previous reports: age, body mass index, donor type, time transplant, and time symptoms to COVID-19 onset, hypertension, diabetes, and baseline eGFR. We used optimal matching on the propensity score (1,2), in which matched strata are formed consisting of either one treated subject and at least one control subject or one control subject and at least one treated subject. We used a ratio of 1:2 (treatment/control). The propensity score was estimated using a probit regression of the treatment on the covariates, which yielded better balance than did a logistic regression. After matching, all standardized mean differences for the covariates were below 0.1 indicating adequate balance (Supplementary Table S2, Supplementary Figures S1 and S2).

Statistical analysis: Continuous data were presented as median and interquartile range (IQR) and compared with Mann-Whitney test. Categorical data was presented in number and percentage and compared with chi-square test or Fisher exact test when appropriate. The Cox proportional hazards model was used to calculate the hazard ratio (HR) and its 95% confidence interval (CI) for the treatment effect between groups in relation to the primary outcome; the proportionality of hazards was evaluated by the correlation tests of Schoenfeld residuals. Secondary outcomes were compared using Fisher exact test. Correlations between the times from onset of symptoms to the convalescent plasma infusion were analyzed using Pearson's coefficient. The analysis was performed using R version 3.6.2. All tests were two-sided, and statistical significance was defined as a p value < 0.05.

References:

1. Hansen, B. B., & Klopfer, S. O. (2006). Optimal Full Matching and Related Designs via Network Flows. Journal of Computational and Graphical Statistics, 15(3), 609–627. doi: 10.1198/106186006X137047

2. Ho, D. E., Imai, K., King, G., & Stuart, E. A. (2011). MatchIt: Nonparametric Preprocessing for Parametric Causal Inference. Journal of Statistical Software, 42(8). doi:10.18637/jss.v042.i08Adjusted Analysis and Statistics

Missing Data Analysis

Because we had in the majority less than 10% missing data, we chose the listwise deletion. The data pattern of this study suggests missing at random. We also included the missing data in demographic tables.

Supplementary Table S1. Missing Data of all available predictors.

Label	n	Missing n	Missing percent
Id	462	0	0.0
Convalescent plasma	462	0	0.0
Date birth	462	0	0.0
Age	462	0	0.0
Sex	462	0	0.0
Ethnicity	462	0	0.0
Blood group	448	14	3.0
Weight	449	13	2.8
Height	451	11	2.4
BMI (kg/m2)	447	15	3.2
Underlying disease	449	13	2.8
Donor type	449	13	2.8
Prior transplant	447	15	3.2
Date transplant	447	15	3.2
Time transplant	447	15	3.2
Time COVID to symptoms	452	10	2.2
Immunosuppression	459	3	0.6
Steroids use	454	8	1.7
High steroid dose until 3 months	443	19	4.1
Use anti-thymocyte globulin until 3 months	443	19	4.1
Use ACE or ARB	442	20	4.3
Smoking	364	98	21.2
Hypertension	462	0	0.0
Diabetes	462	0	0.0
Auto immune disease	462	0	0.0
Heart disease	462	0	0.0
Pneumopathy	462	0	0.0
Liver disease	462	0	0.0
Past or current neoplasm	462	0	0.0
Creatinine baseline	462	0	0.0
eGFR baseline	461	1	0.2
Date symptom onset	455	7	1.5
Date COVID diagnosis	462	0	0.0

Hospital admission	462	0	0.0
Need use supplementary oxigen	462	0	0.0
Mechanical ventilation	462	0	0.0
Time hospitalization	454	8	1.7
Time death	123	339	73.4+
Death	462	0	0.0
Date convalescent infusion	58	404	87.4*
Plasma ambulatorial hospital	58	404	87.4*
Time between symptoms_and_plasma_infusion	58	404	87.4*
Antibody title	51	411	89.0*

+ only available in patients that experience an event. * only available for convalescent plasma group.

Adjusted Analysis

Balance Measures and Sample Size

Optimal matching on the propensity score with ratio 1:2. The matching is optimal in the sense that that sum of the absolute pairwise distances in the matched sample are as small as possible.

Supplementary Table S2. Balance Measures of propensity score.

	Type	Diff.Un	Diff.Adj
Distance	Distance	NA	0.0219064
Age	Contin.	NA	-0.0577206
BMI category lower 30	Binary	NA	0.0000000
donor_type_deceased_donor	Binary	NA	0.0000000
donor_type_living_donor	Binary	NA	-0.0086207
donor_type_unknown	Binary	NA	0.0086207
time_transplant	Contin.	NA	0.0649490
time_to_symptoms	Contin.	NA	0.0344080
Hypertension	Binary	NA	-0.0603448
diabetes_yes	Binary	NA	0.0258621
eGFR_baseline	Contin.	NA	0.0050320

Supplementary Table 3. Sample Sizes of propensity score.

|	Control	Treated
All	398	58
Matched (ESS)	116	58
Matched (Unweighted)	116	58
Unmatched	206	0
Discarded	76	0

References:

1. Ho, D. E., Imai, K., King, G., & Stuart, E. A. (2011). MatchIt: Nonparametric Preprocessing for Parametric Causal Inference. Journal of Statistical Software, 42(8). doi:10.18637/jss.v042.i08

2. Austin, Peter C. 2011. "An Introduction to Propensity Score Methods for Reducing the Effects of Confounding in Observational Studies." *Multivariate Behavioral Research* 46 (3): 399–424. https://doi.org/10.1080/00273171.2011.568786.

3. Austin, Peter C. 2009. "Balance Diagnostics for Comparing the Distribution of Baseline Covariates Between Treatment Groups in Propensity-Score Matched Samples." *Statistics in Medicine* 28 (25): 3083–3107. https://doi.org/10.1002/sim.3697.

4. Rosenbaum, Paul R., and Donald B. Rubin. 1983. "The Central Role of the Propensity Score in Observational Studies for Causal Effects." *Biometrika* 70 (1): 41–55. https://doi.org/10.1093/biomet/70.1.41.

5. Rubin, Donald B. 1973. "Matching to Remove Bias in Observational Studies." *Biometrics* 29 (1): 159. https://doi.org/10.2307/2529684.

6. Hansen, B. B., & Klopfer, S. O. (2006). Optimal Full Matching and Related Designs via Network Flows. Journal of Computational and Graphical Statistics, 15(3), 609–627. doi: 10.1198/106186006X137047

Covariate Balance

After match, the mean standardized mean differences were below 0.1.

**Supplementary Figure S1. Covariate Balance before (white circles) and after adjusting (black circles).**
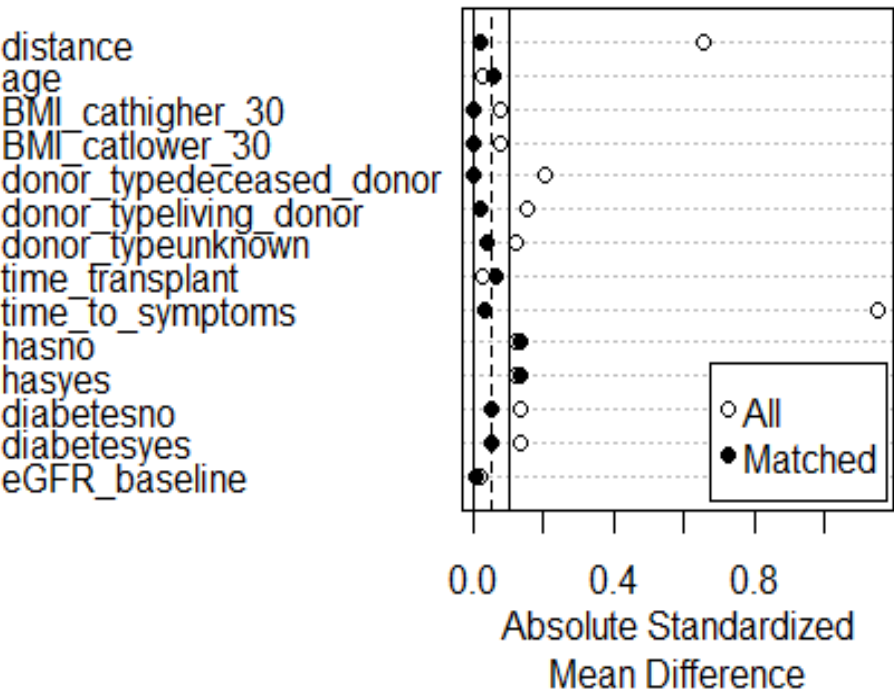
Has yes, presence of hypertension; has no, absence of hypertension.

Plot showing propensity scores in raw data and after match.

The right plots showed the results after match with a similar distribution of propensity scores concentrated in the middle.

Supplementary Figure S2. Propensity Score in raw data and after match.
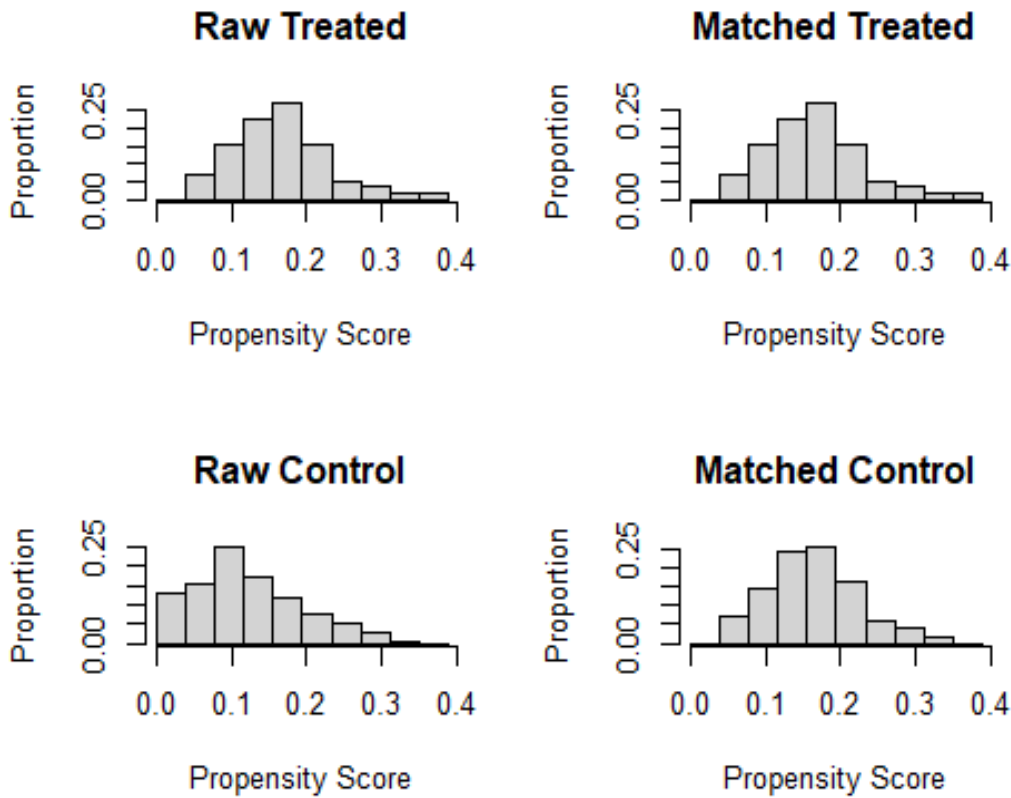
Control: control group; Treated: convalescent plasma

Supplementary Figure S3. Temporal distribution of the 456 patients with confirmed SARS-CoV-2 infection in the year 2021, stratified by convalescent plasma (N = 58, black bars) or unmatched control group (n = 398, light gray bars).